bat will help clarify the physiological basis for male lactation. On theoretical grounds, functional male lactation would be most likely to evolve in monogamous species[1], in which males share in the care of the young and have high certainty of paternity. Studies of the social structure of *D. spadiceus* are required to determine whether they fit these criteria, and whether they actually provide young with milk.

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Antediluvian DNA research

SIR — Lindahl, in a Review article[1] and in Scientific Correspondence[2], has discussed the limitations of techniques to recover DNA from ancient and fossil samples, in this context citing my PCR amplification of part of a chloroplast gene from a 17-million-year-old fossil leaf[3] as being "incompatible with the known properties of the chemical structure of DNA." His criticisms are based on controlled *in vitro* studies of rates of DNA depurination and subsequent chain breakage under physiological solvent conditions under high temperature[4,5]. From these experimental trials, he extrapolated rates of depurination and suggested that they are inconsistent with long-term preservation of DNA. It is unfortunate that Lindahl either ignored or was unaware of various empirical reports that are consistently incompatible with his expected properties of DNA decay. Some of these reports were pointed out by G. Poinar, in a reply to Lindahl's Scientific Correspondence[2].

The most consistent finding from various studies on ancient DNA is that the rate of decay of DNA is not linear over time. Pääbo[6] reported that, in DNA extractions from Mammalian soft tissue ranging in age from 4 to 13,000 years old, the extent of the size reduction of preserved DNA was independent of age, the preponderance of the damage occurring immediately post-mortem due to autolysis. Rapid desiccation appeared to improve preservation, although subsequent oxidative damage to the thymines occurred in all samples over time. The amount of ancient DNA in bones is not appreciably different in 200- and 9,000-year-old samples[7], and DNA preservation in ancient seeds is clearly not linear[8]. Within a shorter time frame, there is variability in DNA preservation which was not correlated with age[9].

Of more direct relevance to the question of preservation of plant fossil DNA from the Clarkia deposits, Soltis *et al.*[10] reported amplification of a 1,320-base pair fragment from a *Taxodium* Clarkia fossil leaf extraction. The analysis of the sequence clearly demonstrated that the sequence was not a contaminant sequence from an extant sample and showed a high degree of similarity to the expected congener.

Lindahl's reference to the work by Sidow *et al.*[11] must also be assessed in its full context. Sidow *et al.* failed to amplify chloroplast sequences from five leaf samples and one acorn, only two of which had DNA that was visible under ethidium bromide staining. They were successful in amplifying a mixed population of apparent bacterial DNA fragments. This success, however, did not correlate with the presence or absence of high molecular mass DNA, as all the samples, including those not having observable DNA and those derived from the adjacent shale without fossil leaf material, could successfully be amplified. The only conclusions that can be drawn from this work are that not all samples are readily amplifiable for chloroplast sequences under the conditions used, and that DNA from soil bacteria is also found in soil-derived samples.

In my view, the most distressing aspect of Lindahl's analysis is his failure to mention that genic DNA contains information that can be analysed by evolutionary systematics. The presence or absence of contaminating DNA is irrelevant to the question of the persistence of fossil DNA, as long as contaminants can be clearly identified. When there is contaminating DNA, analysis of the derived sequence readily identifies the data as false-positive. Even in the few cases in which the contaminating sequence cannot clearly be ascribed to exogenous sources, unexpected phylogenetic relations will indicate a false-positive. It is clear that presently used criteria for validation of ancient DNA are conservative both because of experimental design and because of the stochastic processes of nucleotide substitution, and thus will have a greater tendency towards rejecting true results than towards accepting false-positives[12].

Theory is important for generating testable predictions, and the validity of a theory is determined by how well it is supported by empirical results. The reverse of this process, establishing the validity of empirical results by determining how well they fit theoretical expectations, is at best arrogant, and at worst, regressive. It is clear from a growing body of empirical studies that the preservation of DNA is not simply a function of time. Microenvironmental conditions within preserved tissues and organelles are likely to be vastly different from physiological conditions, making simple extrapolations from *in vitro* studies uninformative.

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Chimpanzee DNA profiles on trial

SIR — The capture and trading of great apes has been banned in 112 countries since a CITES meeting in Washington in 1973. Despite this agreement, about 1,000 chimpanzees are deported annually from Africa to Europe, the United States and Japan[1]. Private owners (zoos, circuses) disguise this illegal trade by simulating births in captivity and by replacing adults with young animals. Measures to identify captive chimpanzees and control their numbers have so far had little effect. Genetic identity tests — the obvious solution — have never been used because of the unavailability of highly polymorphic markers and the inherent difficulties of obtaining blood samples (in most cases, blood is withdrawn under narcosis).

The use of highly polymorphic DNA markers has been proposed[2], in combination with the noninvasive procedures of genomic sampling[3,4]. However, some of these markers (restriction-fragment length polymorphisms, multilocus and single-locus minisatellites) require large amounts of DNA, are labour-intensive and their use as identification profiles is controversial. Others (dinucleotide-repeat microsatellites[5]) are prone to errors in genotype diagnosis. If the standards of reliability and statistical parameters demanded for forensic analyses in humans[6] were adopted for *Pan troglo-*